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Amendments / Listing of Claims

**Claims 1 (Original).** An isolated nucleic acid molecule encoding a carotenoid biosynthetic enzyme, selected from the group consisting of:

- (a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, and 12;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS, 65°C and washed with 2X SSC, 0.1% SDS followed by 0.1X SSC, 0.1% SDS; or
- (c) an isolated nucleic acid molecule that is complementary to (a) or (b).

**Claim 2 (Original).** The isolated nucleic acid molecule of Claim 1 selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, and 11.

**Claim 3 (Original).** An isolated nucleic acid fragment of Claim 1 isolated from *Pectobacterium*.

**Claim 4 (Original).** A polypeptide encoded by the isolated nucleic acid molecule of Claim 1.

**Claim 6-5 (Currently Amended).** The polypeptide of Claim 4 selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, and 12.

**Claim 6 (Original).** An isolated nucleic acid molecule as set forth in SEQ ID NO:18, comprising the *crtE*, *crtX*, *crtY*, *crtI*, *crtB* and *crtZ*, genes or an isolated nucleic acid molecule having at least 95% identity to SEQ ID NO:18, wherein the isolated nucleic acid molecule encodes all of the polypeptides *crtE*, *crtX*, *crtY*, *crtI*, *crtB* and *crtZ*.

**Claim 7 (Original).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a geranylgeranyl pyrophosphate synthase enzyme of at least 301 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO: 2;  
or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 8 (Original).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a zeaxanthin glucosyl transferase enzyme of at least 425 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO: 4;  
or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 9 (Original).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a lycopene cyclase enzyme of at least 388 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO: 6;

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or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 10 (Original).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a phytoene desaturase enzyme of at least 493 amino acids that has at least 81% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO: 8;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 11 (Original).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a phytoene synthase enzyme of at least 309 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO: 10;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 12 (Original).** An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a  $\beta$ -carotene hydroxylase enzyme of at least 178 amino acids that has at least 77% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO: 12;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

**Claim 13 (Original).** A chimeric gene comprising the isolated nucleic acid molecule of any one of Claims 1 or 7-12 operably linked to suitable regulatory sequences.

**Claim 14 (Original).** A vector comprising the isolated nucleic acid molecule of Claim 6.

**Claim 15 (Original).** A transformed host cell comprising the chimeric gene of Claim 12.

**Claim 16 (Original).** A transformed host comprising the isolated nucleic acid molecule of claim 6.

**Claim 17 (Currently Amended).** The transformed host cell of Claim 15 or 16 wherein the host cell is selected from the group consisting of bacteria, yeast, filamentous fungi, algae, and green plants.

**Claim 18 (Original).** The transformed host cell of Claim 17 wherein the host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Yarrowia*, *Rhodospiridium*, *Lipomyces*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Flavobacterium*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Escherichia*, *Pantoea*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylobacterium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*,

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*Thiobacillus, Methanobacterium, Klebsiella, Methylophilus, Methylobacillus, Methylobacterium, Hyphomicrobium, Xanthobacter, Paracoccus, Nocardia, Arthrobacter, Rhodopseudomonas, Torulopsis, Rhodotorula, and Phaffia.*

**Claim 19 (Original).** A method for the production of carotenoid compounds comprising:

- (a) providing a transformed host cell comprising:
  - (i) suitable levels of farnesyl pyrophosphate; and
  - (ii) a set of nucleic acid molecules encoding the enzymes selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, and 12 under the control of suitable regulatory sequences;
- (b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a fermentable carbon substrate whereby a carotenoid compound is produced.

**Claim 20 (Original).** A method for the production of carotenoid compounds comprising:

- (a) providing a transformed host cell comprising:
  - (i) suitable levels of farnesyl pyrophosphate; and
  - (ii) a the isolated nucleic acid molecule of claim 6 under the control of suitable regulatory sequences;
- (b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a fermentable carbon substrate whereby a carotenoid compound is produced.

**Claim 21 (Currently Amended).** A method according to Claim 19 or 20 wherein the transformed host cell is selected from the group consisting of C1 metabolizing hosts, bacteria, yeast, filamentous fungi, algae, and green plants.

**Claim 22 (Currently Amended).** A method according to Claim 19 or 20 wherein the C1 metabolizing host is a methanotroph and the fermentable carbon substrate is selected from the group consisting of methane, methanol, formaldehyde, formic acid, methylated amines, methylated thiols, and carbon dioxide.

**Claim 23 (Original).** A method according to Claim 22 wherein the C1 metabolizing host:

- (a) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and
- (b) comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate-dependent phosphofructokinase enzyme.

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**Claim 24 (Original).** A method according to Claim 23 wherein the C1 metabolizing host cell is a high growth methanotrophic bacterial strain, known as *Methylomonas* 16a and having the ATCC designation PTA 2402.

**Claim 25 (Currently Amended).** A method according to Claim 19 or 20 wherein the transformed host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Yarrowia*, *Rhodospiridium*, *Lipomyces*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Flavobacterium*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Escherichia*, *Pantoea*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, *Methylophilus*, *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, *Torulopsis*, *Rhodotorula*, and *Phaffia*.

**Claim 26 (Currently Amended).** A method according to Claim 19 or 20, wherein the carotenoid compound produced is selected from the group consisting of: antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin,  $\beta$ -cryptoxanthin,  $\alpha$ -carotene,  $\beta$ -carotene, epsilon-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone,  $\gamma$ -carotene, 4-keto- $\gamma$ -carotene,  $\zeta$ -carotene,  $\alpha$ -cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin- $\beta$ -diglucoside, and zeaxanthin.

**Claim 27 (Original).** A method of regulating carotenoid biosynthesis in an organism comprising over-expressing at least one carotenoid gene selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, and 18 in an organism such that the carotenoid biosynthesis is altered in the organism.

**Claim 28 (Original).** A method according to Claim 27 wherein said carotenoid gene is over-expressed on a multicopy plasmid.

**Claim 29 (Original).** A method according to Claim 27 wherein said carotenoid gene is operably linked to an inducible or regulated promoter.

**Claim 30 (Original).** A method according to Claim 27 wherein said carotenoid gene is expressed in antisense orientation.

**Claim 31 (Original).** A method according to Claim 27 wherein said carotenoid gene is disrupted by insertion of foreign DNA into the coding region.

**Claim 32 (Original).** A *Pectobacterium* sp. comprising the 16s rDNA sequence as set forth in SEQ ID NO:16.